

## EXHIBIT 14

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from **NCBI ftp site**

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

☒ Use **Mega BLAST** Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DTGNSFYESTDLTHALSSQFMLSISEASLNQLKSDULDFSGLNVPFYGWQGLWSGWAKIQ
DPEPASSATITDPKANKRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEHYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSPSTKTPLINV
LVPFIGVKGSMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
cttwcqaism rmgyygdrvr orviktovnk eremgeaiag asgnttstis
klvertnpay gkhmqdaemf tnaacmtlni wdrfdvfct1 gatsgylkgn
sasfnlvglf gdgvnatkpa adsignvqln qsvveltydt tawsvgara
alwecgcatl gasfqyaqsk pkieelnvlc naaeftinkp kgyvgkefpl
dltagttaat gtdasidyh ewqaslsly rlnmftpyig vkwsrasfds
dtiriaqprl vtpvvdittl nptiagcgsv agantegqis dtmqivslql
nkmksrkscg iavgttivda dkyavtvetr lideraahvn aqfrf
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**

x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Align**

Sequence 1 lcl|seq\_1 Length 955 **PMPE PTA-2462**

Sequence 2 lcl|seq\_2 Length 394 **MMMA**

No significant similarity was found

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Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

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```
ALSSQPLLSISEASUNQLKRSULMDFSGNLVPHYIGWQGLWIGWARTQDFEASSATITUMQ  
KANRFHRTLTLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSELTTPSDHPFWGIT  
GGGLGMMVYQDFRENHGPFGHMRSSGYSAGMIAGQTHFSLKFSQTYTKLNERYAKNNVSSK  
NYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYTQGENLTSQGTFRSQTMGGAVFFDL  
PMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMMNAT  
QRPOAWTVELAYQPVLYRQEPGIATQLLASKGIWFGSGSPSSRHAMSYKISQQTQPLSWLT  
LHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
cttwcqaism rmgyygarvr orviktavnk eremgeaiag asgnttctis  
klvertnpay gkhmqdaemf tnaacmtlni wdrfdvftcl gatsgylkgn  
sasfnlvglf gdgvnatkpa adsipnvqln qsvveltydt tawsvgara  
alwecgcatl gasfyaqsk pkieelnvlc naaeflinkp kgyvgkefpl  
dltagttaat gtkdasidyh ewqaslsly rlnmftpyig vkwsrasfds  
dtiriaqprl vtpvvdittl nptiagcgsv agantegqis dtmqivslql  
nkmsrkscg iavgttivda dkyavtvetr lideraahvn aqgrf
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Low-complexity**Sequence 1 lcl|seq\_1 Length 965 *SEA ID NO: 2*Sequence 2 lcl|seq\_2 Length 394 *COMP*

No significant similarity was found